

SEQUENCE LISTING

<110> Valenzuela et al., David M.

<120> NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS

<130> REG 195-BZ

<140> Not yet known
<141> Filed herewith

<150> 09/077,955
<151> 1998-09-10

<150> PCT/US96/20696
<151> 1996-12-13

<150> 08/644,271
<151> 1996-05-10

<150> 60/008,657
<151> 1995-12-15

<160> 36

<170> PatentIn Ver. 2.0

<210> 1
<211> 868
<212> PRT
<213> Rattus sp.

<400> 1
Met Arg Glu Leu Val Asn Ile Pro Leu Leu Gln Met Leu Thr Leu Val
1 5 10 15
Ala Phe Ser Gly Thr Glu Lys Leu Pro Lys Ala Pro Val Ile Thr Thr
20 25 30
Pro Leu Glu Thr Val Asp Ala Leu Val Glu Glu Val Ala Thr Phe Met
35 40 45
Cys Ala Val Glu Ser Tyr Pro Gln Pro Glu Ile Ser Trp Thr Arg Asn
50 55 60
Lys Ile Leu Ile Lys Leu Phe Asp Thr Arg Tyr Ser Ile Arg Glu Asn
65 70 75 80
Gly Gln Leu Leu Thr Ile Leu Ser Val Glu Asp Ser Asp Asp Gly Ile
85 90 95
Tyr Cys Cys Thr Ala Asn Asn Gly Val Gly Gly Ala Val Glu Ser Cys
100 105 110
Gly Ala Leu Gln Val Lys Met Lys Pro Lys Ile Thr Arg Pro Pro Ile
115 120 125
Asn Val Lys Ile Ile Glu Gly Leu Lys Ala Val Leu Pro Cys Thr Thr
130 135 140

Met Gly Asn Pro Lys Pro Ser Val Ser Trp Ile Lys Gly Asp Ser Ala
 145 150 155 160
 Leu Arg Glu Asn Ser Arg Ile Ala Val Leu Glu Ser Gly Ser Leu Arg
 165 170 175
 Ile His Asn Val Gln Lys Glu Asp Ala Gly Gln Tyr Arg Cys Val Ala
 180 185 190
 Lys Asn Ser Leu Gly Thr Ala Tyr Ser Lys Leu Val Lys Leu Glu Val
 195 200 205
 Glu Val Phe Ala Arg Ile Leu Arg Ala Pro Glu Ser His Asn Val Thr
 210 215 220
 Phe Gly Ser Phe Val Thr Leu Arg Cys Thr Ala Ile Gly Met Pro Val
 225 230 235 240
 Pro Thr Ile Ser Trp Ile Glu Asn Gly Asn Ala Val Ser Ser Gly Ser
 245 250 255
 Ile Gln Glu Asn Val Lys Asp Arg Val Ile Asp Ser Arg Leu Gln Leu
 260 265 270
 Phe Ile Thr Lys Pro Gly Leu Tyr Thr Cys Ile Ala Thr Asn Lys His
 275 280 285
 Gly Glu Lys Phe Ser Thr Ala Lys Ala Ala Ala Thr Val Ser Ile Ala
 290 295 300
 Glu Trp Ser Lys Ser Gln Lys Glu Ser Lys Gly Tyr Cys Ala Gln Tyr
 305 310 315 320
 Arg Gly Glu Val Cys Asp Ala Val Leu Val Lys Asp Ser Leu Val Phe
 325 330 335
 Phe Asn Thr Ser Tyr Pro Asp Pro Glu Glu Ala Gln Glu Leu Leu Ile
 340 345 350
 His Thr Ala Trp Asn Glu Leu Lys Ala Val Ser Pro Leu Cys Arg Pro
 355 360 365
 Ala Ala Glu Ala Leu Leu Cys Asn His Leu Phe Gln Glu Cys Ser Pro
 370 375 380
 Gly Val Leu Pro Thr Pro Met Pro Ile Cys Arg Glu Tyr Cys Leu Ala
 385 390 395 400
 Val Lys Glu Leu Phe Cys Ala Lys Glu Trp Leu Ala Met Glu Gly Lys
 405 410 415
 Thr His Arg Gly Leu Tyr Arg Ser Gly Met His Phe Leu Pro Val Pro
 420 425 430
 Glu Cys Ser Lys Leu Pro Ser Met His Gln Asp Pro Thr Ala Cys Thr
 435 440 445
 Arg Leu Pro Tyr Leu Asp Tyr Lys Lys Glu Asn Ile Thr Thr Phe Pro
 450 455 460

Ser Ile Thr Ser Ser Lys Pro Ser Val Asp Ile Pro Asn Leu Pro Ala
 465 470 475 480
 Ser Thr Ser Ser Phe Ala Val Ser Pro Ala Tyr Ser Met Thr Val Ile
 485 490 495
 Ile Ser Ile Met Ser Cys Phe Ala Val Phe Ala Leu Leu Thr Ile Thr
 500 505 510
 Thr Leu Tyr Cys Cys Arg Arg Arg Arg Glu Trp Lys Asn Lys Lys Arg
 515 520 525
 Glu Ser Ala Ala Val Thr Leu Thr Thr Leu Pro Ser Glu Leu Leu Leu
 530 535 540
 Asp Arg Leu His Pro Asn Pro Met Tyr Gln Arg Met Pro Leu Leu Leu
 545 550 555 560
 Asn Pro Lys Leu Leu Ser Leu Glu Tyr Pro Arg Asn Asn Ile Glu Tyr
 565 570 575
 Val Arg Asp Ile Gly Glu Gly Ala Phe Gly Arg Val Phe Gln Ala Arg
 580 585 590
 Ala Pro Gly Leu Leu Pro Tyr Glu Pro Phe Thr Met Val Ala Val Lys
 595 600 605
 Met Leu Lys Glu Glu Ala Ser Ala Asp Met Gln Ala Asp Phe Gln Arg
 610 615 620
 Glu Ala Ala Leu Met Ala Glu Phe Asp Asn Pro Asn Ile Val Lys Leu
 625 630 635 640
 Leu Gly Val Cys Ala Val Gly Lys Pro Met Cys Leu Leu Phe Glu Tyr
 645 650 655
 Met Ala Tyr Gly Asp Leu Asn Glu Phe Leu Arg Ser Met Ser Pro His
 660 665 670
 Thr Val Cys Ser Leu Ser His Ser Asp Leu Ser Thr Arg Ala Arg Val
 675 680 685
 Ser Ser Pro Gly Pro Pro Leu Ser Cys Ala Glu Gln Leu Cys Ile
 690 695 700
 Ala Arg Gln Val Ala Ala Gly Met Ala Tyr Leu Ser Glu Arg Lys Phe
 705 710 715 720
 Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Met
 725 730 735
 Val Val Lys Ile Ala Asp Phe Gly Leu Ser Arg Asn Ile Tyr Ser Ala
 740 745 750
 Asp Tyr Tyr Lys Ala Asp Gly Asn Asp Ala Ile Pro Ile Arg Trp Met
 755 760 765
 Pro Pro Glu Ser Ile Phe Tyr Asn Arg Tyr Thr Thr Glu Ser Asp Val
 770 775 780

Trp Ala Tyr Gly Val Val Leu Trp Glu Ile Phe Ser Tyr Gly Leu Gln
 785 790 795 800

Pro Tyr Tyr Gly Met Ala His Glu Glu Val Ile Tyr Tyr Val Arg Asp
 805 810 815

Gly Asn Ile Leu Ala Cys Pro Glu Asn Cys Pro Leu Glu Leu Tyr Asn
 820 825 830

Leu Met Arg Leu Cys Trp Ser Lys Leu Pro Ala Asp Arg Pro Ser Phe
 835 840 845

Cys Ser Ile His Arg Ile Leu Gln Arg Met Cys Glu Arg Ala Glu Gly
 850 855 860

Thr Val Gly Val
 865

<210> 2
 <211> 2869
 <212> DNA
 <213> Rattus sp.

<220>
 <221> modified_base
 <222> (2817)
 <223> n=a, c, g, or t

<220>
 <221> modified_base
 <222> (2823)
 <223> n=a, c, g, or t

<220>
 <221> modified_base
 <222> (2824)
 <223> n=a, c, g, or t

<220>
 <221> modified_base
 <222> (2867)
 <223> n=a, c, g, or t

<400> 2
 gaattcggca cgagcaaaca gtcatttagtg gacgactcta ttgtataaaa ctgtgcttta 60
 aaatgtaaac cagggagcgt ttttttcct cacattgtcc agaagcaacc ttttttcctg 120
 agcctggatt aatcatgaga gagctcgta acattccact gttacagatg ctcaccctgg 180
 ttgccttcag cgggaccggag aaacttccaa aagccctgt catcaccacg cctcttgaaa 240
 ctgttagatgc cttagttgaa gaagtggcga ctttcatgtg cggccgtggaa tcctaccctc 300
 agcctgaaat ttcttgacc agaaataaaa ttctcatcaa gctgtttgac acccgctaca 360
 gcatccgaga gaacggtcag ctcctcacca tcctgagtgt ggaggacagt gatgatggca 420
 tctactgctg cacagccaaac aatggagtttgg gaggagcgtt gaaaaattgt ggcgcctgc 480
 aagtgaagat gaagcctaaa ataactcgta ctcctcacca tgtaaaaaata attgaggat 540
 tgaaaaggcgt cctaccgtgc actacgatgg gtaaccccaa gccatccgtg tcctggatta 600
 agggggacag tgctctcagg gaaaattcca ggattgcagt tcttgaatct gggagttaa 660
 ggatccataa tgtgcaaaag gaagacgcag gacagtaccg atgtgtggca aaaaacagcc 720
 tgggcacagc ttactccaaa ctggtgaagc tggaaagtgg a gtttttgca agaattcctgc 780
 gtgctcctga atccccacaat gtcacctttg gttcctttgt aaccctacgc tgcacagcaa 840
 taggcattgcc tgtccccacc atcagctgga ttgaaaacgg aaatgctgtt ttttcaggtt 900
 ccattcaaga gaatgtgaaa gaccgagtgta ttgactcaag actccagctc tttatcacaa 960

agccaggact ctacacatgc atagctacca ataagcatgg agagaaaattc agtaccgcaa 1020
 aggctgcgc cactgtcagt atagcagaat ggagcaaatc acagaaaagaa agcaaaggct 1080
 actgtgccc gtacagaggg gaggtgtgtg atgcgcgtcct ggtgaaaagac tctcttgtct 1140
 tcttcaacac ctcctatccc gaccctgagg aggcccaaga gctgctgatc cacactgcgt 1200
 ggaatgaact caaggctgtg agcccactct gccgaccagc tgccgaggct ctgctgtgta 1260
 atcaccttcc caggaggtgc agccctggag tgctacctac tccatgccc atttgcagag 1320
 agtactgctt ggcagtaaag gagctttct gtgcaaagga atggctggca atggaaggga 1380
 agacccaccg cggactctac agatccggga tgcatttcct cccggtccc gagtgcagca 1440
 agcttcccag catgcaccag gaccccacag cctgcacaag actgcccgtat ttagattata 1500
 aaaaagaaaa cataacaaca ttcccggtc taacgtcctc caagccgagc gtggacattc 1560
 caaacctgcc tgcctccacg tcttccttcg ccgtctcgcc tgcgtactcc atgactgtca 1620
 tcacatccat catgtcctgc tttgcgggtt ttgcctctct caccatcaact actctctatt 1680
 gctgccgaag gaggagagag tggaaaaata agaaaagaga gtcggcagcg gtgaccctca 1740
 ccacattgcc ttccgagctc ctgctggaca ggctgcattcc caacccatg taccagagga 1800
 tgccactcct tctgaatccc aagttgctca gcctggagta tccgaggaat aacatcgagt 1860
 atgtcagaga catcggagag ggagcgtttt gaagggtctt tcaagcgagg gccccaggct 1920
 tgcttcctta tgaacccttc actatggtgg ctgtgaagat gctgaaggag gaggcctccg 1980
 cagatatgca ggcagacttt cagagggagg cagccctcat ggccggagtt gacaacccca 2040
 acattgtgaa gctcttaggt gtgtgtgctg ttgggaagcc aatgtgcctg ctcttgaat 2100
 atatggccta tggtgacctc aatgagttcc tccgaagcat gtcccccac actgtgtgca 2160
 gcctcagcca cagtgcacgt tccacgaggg ctgcgggtgc cagccctggt cctccacccc 2220
 tgtcttgc ggaacagctc tgtattgcca ggcaagtggc agctggcatg gcctacctgt 2280
 cggagcgc当地 gtttgc当地 cgggacttag ctaccaggaa ctgc当地gggtt ggagagaaca 2340
 tgggtgtaa aattgc当地 ac tttggc当地 ct当地gaacat ctactccgca gactactaca 2400
 aagctgatgg aaacgatgct atacctatcc gctgatgccc acccgagttt atcttctaca 2460
 accgctacac cacggagtca gatgtgtggg cttatggcgt ggtccctctgg gagatcttct 2520
 cctatggact gcagccctac tatggaatgg cccatgagga ggtcatttac tatgtgagag 2580
 atgtaacat cttgc当地 cctgagaact gtcccttggg actgtacaac cttatgc当地 2640
 tatgttggag caagctgc当地 gc当地acacac ccagcttctg cagtatccac cggatc当地 2700
 agcgcatgtg cgagagagca gaggaaacgg taggcgtcta aggttgc当地 tgctcaaaca 2760
 acacccagga ggatcttcc agactgc当地 ctggaggat cctaaacagc agggcgnata 2820
 agnncagata ggaagagttt atctcaggca gcacgtnac ttggttt 2869

<210> 3

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

Asp Val Trp Ala Tyr Gly

1 5

<210> 4

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> modified_base

<222> (18)

<223> n=a, c, g, or t

<220>

<221> modified_base

<222> (24)
 <223> n=a, c, g, or t

<400> 4
 gaattcgagc tcccrwangc ccanacrtc

29

<210> 5
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 5
 Asp Leu Ala Thr Arg Asn
 1 5

<210> 6
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> modified_base
 <222> (17)
 <223> n=a, c, g, or t

<220>
 <221> modified_base
 <222> (20)
 <223> n=a, c, g, or t

<220>
 <221> modified_base
 <222> (23)
 <223> n=a, c, g, or t

<220>
 <221> modified_base
 <222> (26)
 <223> n=a, c, g, or t

<400> 6
 tcttgactcg agayytngcn acnmgnaa

28

<210> 7
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 7
 Asp Leu Ala Ala Arg Asn
 1 5

```

<210> 8
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> modified_base
<222> (17)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (20)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (23)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (26)
<223> n=a, c, g, or t

<400> 8
tcttgactcg agayytngcn gcnmgnaa 28

<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 9
Asp Val Trp Ser Leu Gly
 1           5

<210> 10
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> modified_base
<222> (6)
<223> n=a, c, g, or t

<220>
<221> modified_base

```

<222> (12)
<223> n=a, c, g, or t

<400> 10
ctrccanaccw snatrcctc gagcttaag

29

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
Asp Val Trp Ser Phe Gly
1 5

<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> modified_base
<222> (6)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (11)
<223> n=a, c, g, or t

<400> 12
ctrccanaccw snaarccctc gagcttaag

29

<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
Asp Val Trp Ser Tyr Gly
1 5

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
 <221> modified_base
 <222> (6)
 <223> n=a, c, g, or t

<220>
 <221> modified_base
 <222> (12)
 <223> n=a, c, g, or t

<220>
 <221> modified_base
 <222> (15)
 <223> n=a, c, g, or t

<400> 14
 ctrcanaccw snrancctc gagcttaag

29

<210> 15
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> modified_base
 <222> (18)
 <223> n=a, c, g, or t

<220>
 <221> modified_base
 <222> (24)
 <223> n=a, c, g, or t

<400> 15
 gaattcgagc tcccransw ccanacrtc

29

<210> 16
 <211> 18
 <212> PRT
 <213> Gallus gallus

<400> 16
 Thr Leu Pro Ser Glu Leu Leu Leu Asp Arg Leu His Pro Asn Pro Met
 1 5 10 15

Tyr Gln

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 17	
gacgacacctct tccggaattc	20
<210> 18	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 18	
gtgcacatcc acaatggc	18
<210> 19	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 19	
gagcagaggg aaggttccct g	21
<210> 20	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 20	
tcattgtccc agctgcgtgg	20
<210> 21	
<211> 41	
<212> DNA	
<213> Homo sapiens	
<400> 21	
gagagaggtt taaacatgag cccctgccag cccaaacccct g	41
<210> 22	
<211> 39	
<212> DNA	
<213> Homo sapiens	
<400> 22	
ctctgcggcc gcttatcatg gggtggggca gggccgcag	39
<210> 23	
<211> 49	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	

<400> 23
 gatatctctcg agaaaagaga ggctgaagct agccctgcc agcccaacc 49

 <210> 24
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 24
 aatagtgcgg ccgccaacac tcaggcaaga aaatcatatc 40

 <210> 25
 <211> 456
 <212> PRT
 <213> Homo sapiens

 <400> 25
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Asp
 1 5 10 15

 Tyr Lys Asp Asp Asp Asp Lys Gln Thr Ala Ser Gly Gln Asp Gly Ser
 20 25 30

 Gly Pro Phe Leu Ala Asp Phe Asn Gly Phe Ser His Leu Glu Leu Arg
 35 40 45

 Gly Leu His Thr Phe Ala Arg Asp Leu Gly Glu Lys Met Ala Leu Glu
 50 55 60

 Val Val Phe Leu Ala Arg Gly Pro Ser Gly Leu Leu Tyr Asn Gly
 65 70 75 80

 Gln Lys Thr Asp Gly Lys Gly Asp Phe Val Ser Leu Ala Leu Arg Asp
 85 90 95

 Arg Arg Leu Glu Phe Arg Tyr Asp Leu Gly Lys Gly Ala Ala Val Ile
 100 105 110

 Arg Ser Arg Glu Pro Val Thr Leu Gly Ala Trp Thr Arg Val Ser Leu
 115 120 125

 Glu Arg Asn Gly Arg Lys Gly Ala Leu Arg Val Gly Asp Gly Pro Arg
 130 135 140

 Val Leu Gly Glu Ser Pro Lys Ser Arg Lys Val Pro His Thr Val Leu
 145 150 155 160

 Asn Leu Lys Glu Pro Leu Tyr Val Gly Gly Ala Pro Asp Phe Ser Lys
 165 170 175

 Leu Ala Arg Ala Ala Ala Val Ser Ser Gly Phe Asp Gly Ala Ile Gln
 180 185 190

 Leu Val Ser Leu Gly Gly Arg Gln Leu Leu Thr Pro Glu His Val Leu
 195 200 205

 Arg Gln Val Asp Val Thr Ser Phe Ala Gly His Pro Cys Thr Arg Ala
 210 215 220

Ser Gly His Pro Cys Leu Asn Gly Ala Ser Cys Val Pro Arg Glu Ala
 225 230 235 240
 Ala Tyr Val Cys Leu Cys Pro Gly Gly Phe Ser Gly Pro His Cys Glu
 245 250 255
 Lys Gly Leu Val Glu Lys Ser Ala Gly Asp Val Asp Thr Leu Ala Phe
 260 265 270
 Asp Gly Arg Thr Phe Val Glu Tyr Leu Asn Ala Val Thr Glu Ser Glu
 275 280 285
 Leu Ala Asn Glu Ile Pro Val Glu Lys Ala Leu Gln Ser Asn His Phe
 290 295 300
 Glu Leu Ser Leu Arg Thr Glu Ala Thr Gln Gly Leu Val Leu Trp Ser
 305 310 315 320
 Gly Lys Ala Thr Glu Arg Ala Asp Tyr Val Ala Leu Ala Ile Val Asp
 325 330 335
 Gly His Leu Gln Leu Ser Tyr Asn Leu Gly Ser Gln Pro Val Val Leu
 340 345 350
 Arg Ser Thr Val Pro Val Asn Thr Asn Arg Trp Leu Arg Val Val Ala
 355 360 365
 His Arg Glu Gln Arg Glu Gly Ser Leu Gln Val Gly Asn Glu Ala Pro
 370 375 380
 Val Thr Gly Ser Ser Pro Leu Gly Ala Thr Gln Leu Asp Thr Asp Gly
 385 390 395 400
 Ala Leu Trp Leu Gly Leu Pro Glu Leu Pro Val Gly Pro Ala Leu
 405 410 415
 Pro Lys Ala Tyr Gly Thr Gly Phe Val Gly Cys Leu Arg Asp Val Val
 420 425 430
 Val Gly Arg His Pro Leu His Leu Leu Glu Asp Ala Val Thr Lys Pro
 435 440 445
 Glu Leu Arg Pro Cys Pro Thr Pro
 450 455

<210> 26
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Asp
 1 5 10 15
 Tyr Lys Asp Asp Asp Asp Lys Asn Gly Phe Ser His Leu Glu Leu Arg
 20 25 30
 Gly Leu His Thr Phe Ala Arg Asp Leu Gly Glu Lys Met Ala Leu Glu
 35 40 45

Val Val Phe Leu Ala Arg Gly Pro Ser Gly Leu Leu Tyr Asn Gly
 50 55 60
 Gln Lys Thr Asp Gly Lys Gly Asp Phe Val Ser Leu Ala Leu Arg Asp
 65 70 75 80
 Arg Arg Leu Glu Phe Arg Tyr Asp Leu Gly Lys Gly Ala Ala Val Ile
 85 90 95
 Arg Ser Arg Glu Pro Val Thr Leu Gly Ala Trp Thr Arg Val Ser Leu
 100 105 110
 Glu Arg Asn Gly Arg Lys Gly Ala Leu Arg Val Gly Asp Gly Pro Arg
 115 120 125
 Val Leu Gly Glu Ser Pro Lys Ser Arg Lys Val Pro His Thr Val Leu
 130 135 140
 Asn Leu Lys Glu Pro Leu Tyr Val Gly Gly Ala Pro Asp Phe Ser Lys
 145 150 155 160
 Leu Ala Arg Ala Ala Ala Val Ser Ser Gly Phe Asp Gly Ala Ile Gln
 165 170 175
 Leu Val Ser Leu Gly Gly Arg Gln Leu Leu Thr Pro Glu His Val Leu
 180 185 190
 Arg Gln Val Asp Val Thr Ser Phe Ala Gly His Pro Cys Thr Arg Ala
 195 200 205
 Ser Gly His Pro Cys Leu Asn Gly Ala Ser Cys Val Pro Arg Glu Ala
 210 215 220
 Ala Tyr Val Cys Leu Cys Pro Gly Gly Phe Ser Gly Pro His Cys Glu
 225 230 235 240
 Lys Gly Leu Val Glu Lys Ser Ala Gly Asp Val Asp Thr Leu Ala Phe
 245 250 255
 Asp Gly Arg Thr Phe Val Glu Tyr Leu Asn Ala Val Thr Glu Ser Glu
 260 265 270
 Leu Ala Asn Glu Ile Pro Val Glu Lys Ala Leu Gln Ser Asn His Phe
 275 280 285
 Glu Leu Ser Leu Arg Thr Glu Ala Thr Gln Gly Leu Val Leu Trp Ser
 290 295 300
 Gly Lys Ala Thr Glu Arg Ala Asp Tyr Val Ala Leu Ala Ile Val Asp
 305 310 315 320
 Gly His Leu Gln Leu Ser Tyr Asn Leu Gly Ser Gln Pro Val Val Leu
 325 330 335
 Arg Ser Thr Val Pro Val Asn Thr Asn Arg Trp Leu Arg Val Val Ala
 340 345 350
 His Arg Glu Gln Arg Glu Gly Ser Leu Gln Val Gly Asn Glu Ala Pro
 355 360 365

Val Thr Gly Ser Ser Pro Leu Gly Ala Thr Gln Leu Asp Thr Asp Gly
 370 375 380

Ala Leu Trp Leu Gly Gly Leu Pro Glu Leu Pro Val Gly Pro Ala Leu
 385 390 395 400

Pro Lys Ala Tyr Gly Thr Gly Phe Val Gly Cys Leu Arg Asp Val Val
 405 410 415

Val Gly Arg His Pro Leu His Leu Leu Glu Asp Ala Val Thr Lys Pro
 420 425 430

Glu Leu Arg Pro Cys Pro Thr Pro
 435 440

<210> 27

<211> 390

<212> PRT

<213> Homo sapiens

<400> 27

Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Asp
 1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Val Ser Leu Ala Leu Arg Asp Arg Arg
 20 25 30

Leu Glu Phe Arg Tyr Asp Leu Gly Lys Gly Ala Ala Val Ile Arg Ser
 35 40 45

Arg Glu Pro Val Thr Leu Gly Ala Trp Thr Arg Val Ser Leu Glu Arg
 50 55 60

Asn Gly Arg Lys Gly Ala Leu Arg Val Gly Asp Gly Pro Arg Val Leu
 65 70 75 80

Gly Glu Ser Pro Lys Ser Arg Lys Val Pro His Thr Val Leu Asn Leu
 85 90 95

Lys Glu Pro Leu Tyr Val Gly Gly Ala Pro Asp Phe Ser Lys Leu Ala
 100 105 110

Arg Ala Ala Ala Val Ser Ser Gly Phe Asp Gly Ala Ile Gln Leu Val
 115 120 125

Ser Leu Gly Gly Arg Gln Leu Leu Thr Pro Glu His Val Leu Arg Gln
 130 135 140

Val Asp Val Thr Ser Phe Ala Gly His Pro Cys Thr Arg Ala Ser Gly
 145 150 155 160

His Pro Cys Leu Asn Gly Ala Ser Cys Val Pro Arg Glu Ala Ala Tyr
 165 170 175

Val Cys Leu Cys Pro Gly Gly Phe Ser Gly Pro His Cys Glu Lys Gly
 180 185 190

Leu Val Glu Lys Ser Ala Gly Asp Val Asp Thr Leu Ala Phe Asp Gly
 195 200 205

Arg Thr Phe Val Glu Tyr Leu Asn Ala Val Thr Glu Ser Glu Leu Ala
 210 215 220
 Asn Glu Ile Pro Val Glu Lys Ala Leu Gln Ser Asn His Phe Glu Leu
 225 230 235 240
 Ser Leu Arg Thr Glu Ala Thr Gln Gly Leu Val Leu Trp Ser Gly Lys
 245 250 255
 Ala Thr Glu Arg Ala Asp Tyr Val Ala Leu Ala Ile Val Asp Gly His
 260 265 270
 Leu Gln Leu Ser Tyr Asn Leu Gly Ser Gln Pro Val Val Leu Arg Ser
 275 280 285
 Thr Val Pro Val Asn Thr Asn Arg Trp Leu Arg Val Val Ala His Arg
 290 295 300
 Glu Gln Arg Glu Gly Ser Leu Gln Val Gly Asn Glu Ala Pro Val Thr
 305 310 315 320
 Gly Ser Ser Pro Leu Gly Ala Thr Gln Leu Asp Thr Asp Gly Ala Leu
 325 330 335
 Trp Leu Gly Gly Leu Pro Glu Leu Pro Val Gly Pro Ala Leu Pro Lys
 340 345 350
 Ala Tyr Gly Thr Gly Phe Val Gly Cys Leu Arg Asp Val Val Val Gly
 355 360 365
 Arg His Pro Leu His Leu Leu Glu Asp Ala Val Thr Lys Pro Glu Leu
 370 375 380
 Arg Pro Cys Pro Thr Pro
 385 390

 <210> 28
 <211> 338
 <212> PRT
 <213> Homo sapiens

 <400> 28
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Asp
 1 5 10 15
 Tyr Lys Asp Asp Asp Asp Lys Gly Pro Arg Val Leu Gly Glu Ser Pro
 20 25 30
 Lys Ser Arg Lys Val Pro His Thr Val Leu Asn Leu Lys Glu Pro Leu
 35 40 45
 Tyr Val Gly Gly Ala Pro Asp Phe Ser Lys Leu Ala Arg Ala Ala Ala
 50 55 60
 Val Ser Ser Gly Phe Asp Gly Ala Ile Gln Leu Val Ser Leu Gly Gly
 65 70 75 80
 Arg Gln Leu Leu Thr Pro Glu His Val Leu Arg Gln Val Asp Val Thr
 85 90 95

Ser Phe Ala Gly His Pro Cys Thr Arg Ala Ser Gly His Pro Cys Leu
 100 105 110
 Asn Gly Ala Ser Cys Val Pro Arg Glu Ala Ala Tyr Val Cys Leu Cys
 115 120 125
 Pro Gly Gly Phe Ser Gly Pro His Cys Glu Lys Gly Leu Val Glu Lys
 130 135 140
 Ser Ala Gly Asp Val Asp Thr Leu Ala Phe Asp Gly Arg Thr Phe Val
 145 150 155 160
 Glu Tyr Leu Asn Ala Val Thr Glu Ser Glu Leu Ala Asn Glu Ile Pro
 165 170 175
 Val Glu Lys Ala Leu Gln Ser Asn His Phe Glu Leu Ser Leu Arg Thr
 180 185 190
 Glu Ala Thr Gln Gly Leu Val Leu Trp Ser Gly Lys Ala Thr Glu Arg
 195 200 205
 Ala Asp Tyr Val Ala Leu Ala Ile Val Asp Gly His Leu Gln Leu Ser
 210 215 220
 Tyr Asn Leu Gly Ser Gln Pro Val Val Leu Arg Ser Thr Val Pro Val
 225 230 235 240
 Asn Thr Asn Arg Trp Leu Arg Val Val Ala His Arg Glu Gln Arg Glu
 245 250 255
 Gly Ser Leu Gln Val Gly Asn Glu Ala Pro Val Thr Gly Ser Ser Pro
 260 265 270
 Leu Gly Ala Thr Gln Leu Asp Thr Asp Gly Ala Leu Trp Leu Gly Gly
 275 280 285
 Leu Pro Glu Leu Pro Val Gly Pro Ala Leu Pro Lys Ala Tyr Gly Thr
 290 295 300
 Gly Phe Val Gly Cys Leu Arg Asp Val Val Val Gly Arg His Pro Leu
 305 310 315 320
 His Leu Leu Glu Asp Ala Val Thr Lys Pro Glu Leu Arg Pro Cys Pro
 325 330 335
 Thr Pro

<210> 29
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 29
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Asp
 1 5 10 15
 Tyr Lys Asp Asp Asp Asp Lys Gly Phe Asp Gly Ala Ile Gln Leu Val
 20 25 30

Ser Leu Gly Gly Arg Gln Leu Leu Thr Pro Glu His Val Leu Arg Gln
 35 40 45
 Val Asp Val Thr Ser Phe Ala Gly His Pro Cys Thr Arg Ala Ser Gly
 50 55 60
 His Pro Cys Leu Asn Gly Ala Ser Cys Val Pro Arg Glu Ala Ala Tyr
 65 70 75 80
 Val Cys Leu Cys Pro Gly Gly Phe Ser Gly Pro His Cys Glu Lys Gly
 85 90 95
 Leu Val Glu Lys Ser Ala Gly Asp Val Asp Thr Leu Ala Phe Asp Gly
 100 105 110
 Arg Thr Phe Val Glu Tyr Leu Asn Ala Val Thr Glu Ser Glu Leu Ala
 115 120 125
 Asn Glu Ile Pro Val Glu Lys Ala Leu Gln Ser Asn His Phe Glu Leu
 130 135 140
 Ser Leu Arg Thr Glu Ala Thr Gln Gly Leu Val Leu Trp Ser Gly Lys
 145 150 155 160
 Ala Thr Glu Arg Ala Asp Tyr Val Ala Leu Ala Ile Val Asp Gly His
 165 170 175
 Leu Gln Leu Ser Tyr Asn Leu Gly Ser Gln Pro Val Val Leu Arg Ser
 180 185 190
 Thr Val Pro Val Asn Thr Asn Arg Trp Leu Arg Val Val Ala His Arg
 195 200 205
 Glu Gln Arg Glu Gly Ser Leu Gln Val Gly Asn Glu Ala Pro Val Thr
 210 215 220
 Gly Ser Ser Pro Leu Gly Ala Thr Gln Leu Asp Thr Asp Gly Ala Leu
 225 230 235 240
 Trp Leu Gly Gly Leu Pro Glu Leu Pro Val Gly Pro Ala Leu Pro Lys
 245 250 255
 Ala Tyr Gly Thr Gly Phe Val Gly Cys Leu Arg Asp Val Val Val Gly
 260 265 270
 Arg His Pro Leu His Leu Leu Glu Asp Ala Val Thr Lys Pro Glu Leu
 275 280 285
 Arg Pro Cys Pro Thr Pro
 290

<210> 30
 <211> 256
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Asp
 1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Ala Ser Gly His Pro Cys Leu Asn Gly
 20 25 30

Ala Ser Cys Val Pro Arg Glu Ala Ala Tyr Val Cys Leu Cys Pro Gly
 35 40 45

Gly Phe Ser Gly Pro His Cys Glu Lys Gly Leu Val Glu Lys Ser Ala
 50 55 60

Gly Asp Val Asp Thr Leu Ala Phe Asp Gly Arg Thr Phe Val Glu Tyr
 65 70 75 80

Leu Asn Ala Val Thr Glu Ser Glu Leu Ala Asn Glu Ile Pro Val Glu
 85 90 95

Lys Ala Leu Gln Ser Asn His Phe Glu Leu Ser Leu Arg Thr Glu Ala
 100 105 110

Thr Gln Gly Leu Val Leu Trp Ser Gly Lys Ala Thr Glu Arg Ala Asp
 115 120 125

Tyr Val Ala Leu Ala Ile Val Asp Gly His Leu Gln Leu Ser Tyr Asn
 130 135 140

Leu Gly Ser Gln Pro Val Val Leu Arg Ser Thr Val Pro Val Asn Thr
 145 150 155 160

Asn Arg Trp Leu Arg Val Val Ala His Arg Glu Gln Arg Glu Gly Ser
 165 170 175

Leu Gln Val Gly Asn Glu Ala Pro Val Thr Gly Ser Ser Pro Leu Gly
 180 185 190

Ala Thr Gln Leu Asp Thr Asp Gly Ala Leu Trp Leu Gly Gly Leu Pro
 195 200 205

Glu Leu Pro Val Gly Pro Ala Leu Pro Lys Ala Tyr Gly Thr Gly Phe
 210 215 220

Val Gly Cys Leu Arg Asp Val Val Val Gly Arg His Pro Leu His Leu
 225 230 235 240

Leu Glu Asp Ala Val Thr Lys Pro Glu Leu Arg Pro Cys Pro Thr Pro
 245 250 255

<210> 31
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 31
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Asp
 1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Ala Gly Asp Val Asp Thr Leu Ala Phe
 20 25 30

Asp Gly Arg Thr Phe Val Glu Tyr Leu Asn Ala Val Thr Glu Ser Glu
 35 40 45

Leu Ala Asn Glu Ile Pro Val Glu Lys Ala Leu Gln Ser Asn His Phe
 50 55 60

Glu Leu Ser Leu Arg Thr Glu Ala Thr Gln Gly Leu Val Leu Trp Ser
 65 70 75 80

Gly Lys Ala Thr Glu Arg Ala Asp Tyr Val Ala Leu Ala Ile Val Asp
 85 90 95

Gly His Leu Gln Leu Ser Tyr Asn Leu Gly Ser Gln Pro Val Val Leu
 100 105 110

Arg Ser Thr Val Pro Val Asn Thr Asn Arg Trp Leu Arg Val Val Ala
 115 120 125

His Arg Glu Gln Arg Glu Gly Ser Leu Gln Val Gly Asn Glu Ala Pro
 130 135 140

Val Thr Gly Ser Ser Pro Leu Gly Ala Thr Gln Leu Asp Thr Asp Gly
 145 150 155 160

Ala Leu Trp Leu Gly Gly Leu Pro Glu Leu Pro Val Gly Pro Ala Leu
 165 170 175

Pro Lys Ala Tyr Gly Thr Gly Phe Val Gly Cys Leu Arg Asp Val Val
 180 185 190

Val Gly Arg His Pro Leu His Leu Leu Glu Asp Ala Val Thr Lys Pro
 195 200 205

Glu Leu Arg Pro Cys Pro Thr Pro
 210 215

<210> 32

<211> 2610

<212> DNA

<213> Homo sapiens

<400> 32

atgagagagc tcgtcaacat tccactggta cataattctta ctctgggtgc cttcagcgga 60
 actgagaaac ttccaaaagc tcctgtcatc accactcctc ttgaaacagt ggatgcctta 120
 gttgaagaag tggctacttt catgtgtgca gtggaatcct acccccagcc tgagattcc 180
 tggactagaa ataaaattct cattaaactc tttgacaccc ggtacagcat cccggagaat 240
 gggcagctcc tcaccatcct gagtgtggaa gacagtgtat atggcattta ctgctgcacg 300
 gccaacaatg gtgtgggagg agctgtggag agttgtggag ccctgcaagt gaagatgaaa 360
 cctaaaataa ctcgcccctcc cataaatgtg aaaataatag agggattaaa agcagtccta 420
 ccatgtacta caatggtaa tcccaaaccat tcagtgtctt ggataaaagg agacagccct 480
 ctcagggaaa attcccaaat tgcagttctt gaatctggaa gcttgaggat tcataacgta 540
 caaaaaggaaat atgcaggaca gtatcgatgt gtggcaaaaa acagcctcgg gacagcatat 600
 tccaaagtgg tgaagctgga agttgaggtt tttgccagga tcctgcgggc tcctgaatcc 660
 cacaatgtca cctttggctc ctttgtgacc ctgcactgtat cagcaacagg cattcctgtc 720
 cccaccatca cctggattga aaacggaaat gctgtttctt ctgggtccat tcaagagagt 780
 gtgaaagacc gagtgattga ctcaagactg cagctgttta tcaccaagcc aggactctac 840
 acatgcatac ctaccaataa gcatggggag aagttcagta ctgccaaggc tgccagccacc 900
 atcagcatac cagaatggag taaaccacag aaagataaca aaggctactg cgccccagtagc 960
 agagggggagg tgtgtaatgc agtcctggca aaagatgctc ttgttttctt caacacactcc 1020
 tatgcggacc ctgaggaggc ccaagagcta ctgggccaca cggcctggaa tgaactgaaa 1080

gtagtgagcc cagtctgccc gccagctgct gaggcttgc tggtaacca catcttccag 1140
 gagtgagtc ctggagtagt gcctactcattt attcccatattt gcagagagta ctgcttggca 1200
 gtaaaggagc tcttctgcgc aaaagaatgg ctggtaatgg aagagaagac ccacagagga 1260
 ctctacagat ccgagatgca tttgctgtcc gtgcagaat gcagcaagct tcccaagcatg 1320
 cattgggacc ccacggcctg tgccagactg ccacatctag attataacaa agaaaaccta 1380
 aaaaacattcc caccatgac gtcctcaaaag ccaagtgtgg acattccaaa tctgccttcc 1440
 tcctcctctt cttccttctc tggtaacccat acataactca tgactgtaat aatctccatc 1500
 atgtccagct ttgcaatatt tggcttctt accataacta ctctctattt ctgcccaga 1560
 agaaaaacaat gaaaaataa gaaaagagaa tcagcagcag taaccctcac cacactgcct 1620
 tctgagctct tactagatag acttcatccc aacccatgt accagaggat gcccgtcctt 1680
 ctgaacccca aattgctcag cttggagtat ccaaggaata acattgaata tggagagac 1740
 atcgaggagg gagcgttgg aagggtgtt caagcaaggg caccaggctt acttccctat 1800
 gaacctttca ctatggtggc agtaaagatg ctcaagaag aagcctcggc agatatgcaa 1860
 gcgacttgc agagggaggc agccctcatg gcagaatttgc acaaccctaa cattgtgaag 1920
 ctattaggag tggtaatgcgtt cgggaagcca atgtgcctgc tctttgaata catggctat 1980
 ggtgacctca atgagttcct cccgagcatg tccctcaca cctgtgcag cctcagtcac 2040
 agtgacttgt ctatggggc tcaggtctcc agccctggc ccccacccct ctcctgtgct 2100
 gagcagcttgc gcatggccag gcaggtggca gtcggcatgg cttacctctc agaacgtaa 2160
 tttgttccacc gagatttgc caccaggaac tggcttggc gcgagaacat ggtggtaaa 2220
 attggccact ttggccctctc caggaacatc tactcagcag actactacaa agctaataa 2280
 aacgacgcta tccctatccg ttggatgcca ccagagtcca tttttataa ccgctacact 2340
 acagagtctg atgtgtggc ctatggcgtg gtcctctgg agatcttctc ctatggcctg 2400
 cagccctact atggatggc ccatgaggag gtcatttact acgtgcgaga tggcaacatc 2460
 ctctcctgccc ctgagaactg cccctggag ctgtacaatc tcatgcgtct atgttgagc 2520
 aagctgcctg cagacagacc cagttcacc agtattcacc gaattctgga acgcatgtgt 2580
 gagagggcag agggaaactgt gaggatctaa 2610

<210> 33
 <211> 869
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Arg Glu Leu Val Asn Ile Pro Leu Val His Ile Leu Thr Leu Val
 1 5 10 15
 Ala Phe Ser Gly Thr Glu Lys Leu Pro Lys Ala Pro Val Ile Thr Thr
 20 25 30
 Pro Leu Glu Thr Val Asp Ala Leu Val Glu Glu Val Ala Thr Phe Met
 35 40 45
 Cys Ala Val Glu Ser Tyr Pro Gln Pro Glu Ile Ser Trp Thr Arg Asn
 50 55 60
 Lys Ile Leu Ile Lys Leu Phe Asp Thr Arg Tyr Ser Ile Arg Glu Asn
 65 70 75 80
 Gly Gln Leu Leu Thr Ile Leu Ser Val Glu Asp Ser Asp Asp Gly Ile
 85 90 95
 Tyr Cys Cys Thr Ala Asn Asn Gly Val Gly Gly Ala Val Glu Ser Cys
 100 105 110
 Gly Ala Leu Gln Val Lys Met Lys Pro Lys Ile Thr Arg Pro Pro Ile
 115 120 125
 Asn Val Lys Ile Ile Glu Gly Leu Lys Ala Val Leu Pro Cys Thr Thr
 130 135 140

Met Gly Asn Pro Lys Pro Ser Val Ser Trp Ile Lys Gly Asp Ser Pro
 145 150 155 160
 Leu Arg Glu Asn Ser Arg Ile Ala Val Leu Glu Ser Gly Ser Leu Arg
 165 170 175
 Ile His Asn Val Gln Lys Glu Asp Ala Gly Gln Tyr Arg Cys Val Ala
 180 185 190
 Lys Asn Ser Leu Gly Thr Ala Tyr Ser Lys Val Val Lys Leu Glu Val
 195 200 205
 Glu Val Phe Ala Arg Ile Leu Arg Ala Pro Glu Ser His Asn Val Thr
 210 215 220
 Phe Gly Ser Phe Val Thr Leu His Cys Thr Ala Thr Gly Ile Pro Val
 225 230 235 240
 Pro Thr Ile Thr Trp Ile Glu Asn Gly Asn Ala Val Ser Ser Gly Ser
 245 250 255
 Ile Gln Glu Ser Val Lys Asp Arg Val Ile Asp Ser Arg Leu Gln Leu
 260 265 270
 Phe Ile Thr Lys Pro Gly Leu Tyr Thr Cys Ile Ala Thr Asn Lys His
 275 280 285
 Gly Glu Lys Phe Ser Thr Ala Lys Ala Ala Ala Thr Ile Ser Ile Ala
 290 295 300
 Glu Trp Ser Lys Pro Gln Lys Asp Asn Lys Gly Tyr Cys Ala Gln Tyr
 305 310 315 320
 Arg Gly Glu Val Cys Asn Ala Val Leu Ala Lys Asp Ala Leu Val Phe
 325 330 335
 Leu Asn Thr Ser Tyr Ala Asp Pro Glu Glu Ala Gln Glu Leu Leu Val
 340 345 350
 His Thr Ala Trp Asn Glu Leu Lys Val Val Ser Pro Val Cys Arg Pro
 355 360 365
 Ala Ala Glu Ala Leu Leu Cys Asn His Ile Phe Gln Glu Cys Ser Pro
 370 375 380
 Gly Val Val Pro Thr Pro Ile Pro Ile Cys Arg Glu Tyr Cys Leu Ala
 385 390 395 400
 Val Lys Glu Leu Phe Cys Ala Lys Glu Trp Leu Val Met Glu Glu Lys
 405 410 415
 Thr His Arg Gly Leu Tyr Arg Ser Glu Met His Leu Leu Ser Val Pro
 420 425 430
 Glu Cys Ser Lys Leu Pro Ser Met His Trp Asp Pro Thr Ala Cys Ala
 435 440 445
 Arg Leu Pro His Leu Asp Tyr Asn Lys Glu Asn Leu Lys Thr Phe Pro
 450 455 460

Pro Met Thr Ser Ser Lys Pro Ser Val Asp Ile Pro Asn Leu Pro Ser
 465 470 475 480
 Ser Ser Ser Ser Ser Phe Ser Val Ser Pro Thr Tyr Ser Met Thr Val
 485 490 495
 Ile Ile Ser Ile Met Ser Ser Phe Ala Ile Phe Val Leu Leu Thr Ile
 500 505 510
 Thr Thr Leu Tyr Cys Cys Arg Arg Arg Lys Gln Trp Lys Asn Lys Lys
 515 520 525
 Arg Glu Ser Ala Ala Val Thr Leu Thr Leu Pro Ser Glu Leu Leu
 530 535 540
 Leu Asp Arg Leu His Pro Asn Pro Met Tyr Gln Arg Met Pro Leu Leu
 545 550 555 560
 Leu Asn Pro Lys Leu Leu Ser Leu Glu Tyr Pro Arg Asn Asn Ile Glu
 565 570 575
 Tyr Val Arg Asp Ile Gly Glu Gly Ala Phe Gly Arg Val Phe Gln Ala
 580 585 590
 Arg Ala Pro Gly Leu Leu Pro Tyr Glu Pro Phe Thr Met Val Ala Val
 595 600 605
 Lys Met Leu Lys Glu Glu Ala Ser Ala Asp Met Gln Ala Asp Phe Gln
 610 615 620
 Arg Glu Ala Ala Leu Met Ala Glu Phe Asp Asn Pro Asn Ile Val Lys
 625 630 635 640
 Leu Leu Gly Val Cys Ala Val Gly Lys Pro Met Cys Leu Leu Phe Glu
 645 650 655
 Tyr Met Ala Tyr Gly Asp Leu Asn Glu Phe Leu Arg Ser Met Ser Pro
 660 665 670
 His Thr Val Cys Ser Leu Ser His Ser Asp Leu Ser Met Arg Ala Gln
 675 680 685
 Val Ser Ser Pro Gly Pro Pro Leu Ser Cys Ala Glu Gln Leu Cys
 690 695 700
 Ile Ala Arg Gln Val Ala Ala Gly Met Ala Tyr Leu Ser Glu Arg Lys
 705 710 715 720
 Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn
 725 730 735
 Met Val Val Lys Ile Ala Asp Phe Gly Leu Ser Arg Asn Ile Tyr Ser
 740 745 750
 Ala Asp Tyr Tyr Lys Ala Asn Glu Asn Asp Ala Ile Pro Ile Arg Trp
 755 760 765
 Met Pro Pro Glu Ser Ile Phe Tyr Asn Arg Tyr Thr Thr Glu Ser Asp
 770 775 780

Val Trp Ala Tyr Gly Val Val Leu Trp Glu Ile Phe Ser Tyr Gly Leu
 785 790 795 800

Gln Pro Tyr Tyr Gly Met Ala His Glu Glu Val Ile Tyr Tyr Val Arg
 805 810 815

Asp Gly Asn Ile Leu Ser Cys Pro Glu Asn Cys Pro Val Glu Leu Tyr
 820 825 830

Asn Leu Met Arg Leu Cys Trp Ser Lys Leu Pro Ala Asp Arg Pro Ser
 835 840 845

Phe Thr Ser Ile His Arg Ile Leu Glu Arg Met Cys Glu Arg Ala Glu
 850 855 860

Gly Thr Val Ser Val
 865

<210> 34
 <211> 1940
 <212> PRT
 <213> Rattus sp.

<400> 34
 Met Pro Pro Leu Pro Leu Glu His Arg Pro Arg Gln Glu Pro Gly Ala
 1 5 10 15

Ser Met Leu Val Arg Tyr Phe Met Ile Pro Cys Asn Ile Cys Leu Ile
 20 25 30

Leu Leu Ala Thr Ser Thr Leu Gly Phe Ala Val Leu Leu Phe Leu Ser
 35 40 45

Asn Tyr Lys Pro Gly Ile His Phe Thr Pro Ala Pro Pro Thr Pro Pro
 50 55 60

Asp Val Cys Arg Gly Met Leu Cys Gly Phe Gly Ala Val Cys Glu Pro
 65 70 75 80

Ser Val Glu Asp Pro Gly Arg Ala Ser Cys Val Cys Lys Lys Asn Ala
 85 90 95

Cys Pro Ala Thr Val Ala Pro Val Cys Gly Ser Asp Ala Ser Thr Tyr
 100 105 110

Ser Asn Glu Cys Glu Leu Gln Arg Ala Gln Cys Asn Gln Gln Arg Arg
 115 120 125

Ile Arg Leu Leu Arg Gln Gly Pro Cys Gly Ser Arg Asp Pro Cys Ala
 130 135 140

Asn Val Thr Cys Ser Phe Gly Ser Thr Cys Val Pro Ser Ala Asp Gly
 145 150 155 160

Gln Thr Ala Ser Cys Leu Cys Pro Thr Thr Cys Phe Gly Ala Pro Asp
 165 170 175

Gly Thr Val Cys Gly Ser Asp Gly Val Asp Tyr Pro Ser Glu Cys Gln
 180 185 190

Leu Leu Ser His Ala Cys Ala Ser Gln Glu His Ile Phe Lys Lys Phe
 195 200 205
 Asn Gly Pro Cys Asp Pro Cys Gln Gly Ser Met Ser Asp Leu Asn His
 210 215 220
 Ile Cys Arg Val Asn Pro Arg Thr Arg His Pro Glu Met Leu Leu Arg
 225 230 235 240
 Pro Glu Asn Cys Pro Ala Gln His Thr Pro Ile Cys Gly Asp Asp Gly
 245 250 255
 Val Thr Tyr Glu Asn Asp Cys Val Met Ser Arg Ile Gly Ala Thr Arg
 260 265 270
 Gly Leu Leu Leu Gln Lys Val Arg Ser Gly Gln Cys Gln Thr Arg Asp
 275 280 285
 Gln Cys Pro Glu Thr Cys Gln Phe Asn Ser Val Cys Leu Ser Arg Arg
 290 295 300
 Gly Arg Pro His Cys Ser Cys Asp Arg Val Thr Cys Asp Gly Ser Tyr
 305 310 315 320
 Arg Pro Val Cys Ala Gln Asp Gly His Thr Tyr Asn Asn Asp Cys Trp
 325 330 335
 Arg Gln Gln Ala Glu Cys Arg Gln Gln Arg Ala Ile Pro Pro Lys His
 340 345 350
 Gln Gly Pro Cys Asp Gln Thr Pro Ser Pro Cys His Gly Val Gln Cys
 355 360 365
 Ala Phe Gly Ala Val Cys Thr Val Lys Asn Gly Lys Ala Glu Cys Glu
 370 375 380
 Cys Gln Arg Val Cys Ser Gly Ile Tyr Asp Pro Val Cys Gly Ser Asp
 385 390 395 400
 Gly Val Thr Tyr Gly Ser Val Cys Glu Leu Glu Ser Met Ala Cys Thr
 405 410 415
 Leu Gly Arg Glu Ile Gln Val Ala Arg Arg Gly Pro Cys Asp Pro Cys
 420 425 430
 Gly Gln Cys Arg Phe Gly Ser Leu Cys Glu Val Glu Thr Gly Arg Cys
 435 440 445
 Val Cys Pro Ser Glu Cys Val Glu Ser Ala Gln Pro Val Cys Gly Ser
 450 455 460
 Asp Gly His Thr Tyr Ala Ser Glu Cys Glu Leu His Val His Ala Cys
 465 470 475 480
 Thr His Gln Ile Ser Leu Tyr Val Ala Ser Ala Gly His Cys Gln Thr
 485 490 495
 Cys Gly Glu Lys Val Cys Thr Phe Gly Ala Val Cys Ser Ala Gly Gln
 500 505 510

Cys Val Cys Pro Arg Cys Glu His Pro Pro Pro Gly Pro Val Cys Gly
 515 520 525
 Ser Asp Gly Val Thr Tyr Leu Ser Ala Cys Glu Leu Arg Glu Ala Ala
 530 535 540
 Cys Gln Gln Gln Val Gln Ile Glu Glu Ala His Ala Gly Pro Cys Glu
 545 550 555 560
 Pro Ala Glu Cys Gly Ser Gly Ser Gly Ser Gly Glu Asp Asp Glu
 565 570 575
 Cys Glu Gln Glu Leu Cys Arg Gln Arg Gly Gly Ile Trp Asp Glu Asp
 580 585 590
 Ser Glu Asp Gly Pro Cys Val Cys Asp Phe Ser Cys Gln Ser Val Pro
 595 600 605
 Arg Ser Pro Val Cys Gly Ser Asp Gly Val Thr Tyr Gly Thr Glu Cys
 610 615 620
 Asp Leu Lys Lys Ala Arg Cys Glu Ser Gln Gln Glu Leu Tyr Val Ala
 625 630 635 640
 Ala Gln Gly Ala Cys Arg Gly Pro Thr Leu Ala Pro Leu Leu Pro Val
 645 650 655
 Ala Phe Pro His Cys Ala Gln Thr Pro Tyr Gly Cys Cys Gln Asp Asn
 660 665 670
 Phe Thr Ala Ala Gln Gly Val Gly Leu Ala Gly Cys Pro Ser Thr Cys
 675 680 685
 His Cys Asn Pro His Gly Ser Tyr Ser Gly Thr Cys Asp Pro Ala Thr
 690 695 700
 Gly Gln Cys Ser Cys Arg Pro Gly Val Gly Gly Leu Arg Cys Asp Arg
 705 710 715 720
 Cys Glu Pro Gly Phe Trp Asn Phe Arg Gly Ile Val Thr Asp Gly His
 725 730 735
 Ser Gly Cys Thr Pro Cys Ser Cys Asp Pro Arg Gly Ala Val Arg Asp
 740 745 750
 Asp Cys Glu Gln Met Thr Gly Leu Cys Ser Cys Arg Pro Gly Val Ala
 755 760 765
 Gly Pro Lys Cys Gly Gln Cys Pro Asp Gly Gln Val Leu Gly His Leu
 770 775 780
 Gly Cys Glu Ala Asp Pro Met Thr Pro Val Thr Cys Val Glu Ile His
 785 790 795 800
 Cys Glu Phe Gly Ala Ser Cys Val Glu Lys Ala Gly Phe Ala Gln Cys
 805 810 815
 Ile Cys Pro Thr Leu Thr Cys Pro Glu Ala Asn Ser Thr Lys Val Cys
 820 825 830

Gly Ser Asp Gly Val Thr Tyr Gly Asn Glu Cys Gln Leu Lys Ala Ile
 835 840 845
 Ala Cys Arg Gln Arg Leu Asp Ile Ser Thr Gln Ser Leu Gly Pro Cys
 850 855 860
 Gln Glu Ser Val Thr Pro Gly Ala Ser Pro Thr Ser Ala Ser Met Thr
 865 870 875 880
 Thr Pro Arg His Ile Leu Ser Lys Thr Leu Pro Phe Pro His Asn Ser
 885 890 895
 Leu Pro Leu Ser Pro Gly Ser Thr His Asp Trp Pro Thr Pro Leu
 900 905 910
 Pro Ile Ser Pro His Thr Thr Val Ser Ile Pro Arg Ser Thr Ala Trp
 915 920 925
 Pro Val Leu Thr Val Pro Pro Thr Ala Ala Ala Ser Asp Val Thr Ser
 930 935 940
 Leu Ala Thr Ser Ile Phe Ser Glu Ser Gly Ser Ala Asn Gly Ser Gly
 945 950 955 960
 Asp Glu Glu Leu Ser Gly Asp Glu Glu Ala Ser Gly Gly Ser Gly
 965 970 975
 Gly Leu Glu Pro Pro Val Gly Ser Ile Val Val Thr His Gly Pro Pro
 980 985 990
 Ile Glu Arg Ala Ser Cys Tyr Asn Ser Pro Leu Gly Cys Cys Ser Asp
 995 1000 1005
 Gly Lys Thr Pro Ser Leu Asp Ser Glu Gly Ser Asn Cys Pro Ala Thr
 1010 1015 1020
 Lys Ala Phe Gln Gly Val Leu Glu Leu Glu Gly Val Glu Gly Gln Glu
 1025 1030 1035 1040
 Leu Phe Tyr Thr Pro Glu Met Ala Asp Pro Lys Ser Glu Leu Phe Gly
 1045 1050 1055
 Glu Thr Ala Arg Ser Ile Glu Ser Thr Leu Asp Asp Leu Phe Arg Asn
 1060 1065 1070
 Ser Asp Val Lys Lys Asp Phe Trp Ser Val Arg Leu Arg Glu Leu Gly
 1075 1080 1085
 Pro Gly Lys Leu Val Arg Ala Ile Val Asp Val His Phe Asp Pro Thr
 1090 1095 1100
 Thr Ala Phe Gln Ala Ser Asp Val Gly Gln Ala Leu Leu Arg Gln Ile
 1105 1110 1115 1120
 Gln Val Ser Arg Pro Trp Ala Leu Ala Val Arg Arg Pro Leu Gln Glu
 1125 1130 1135
 His Val Arg Phe Leu Asp Phe Asp Trp Phe Pro Thr Phe Phe Thr Gly
 1140 1145 1150

Ala Ala Thr Gly Thr Thr Ala Ala Met Ala Thr Ala Arg Ala Thr Thr
 1155 1160 1165
 Val Ser Arg Leu Pro Ala Ser Ser Val Thr Pro Arg Val Tyr Pro Ser
 1170 1175 1180
 His Thr Ser Arg Pro Val Gly Arg Thr Thr Ala Pro Pro Thr Thr Arg
 1185 1190 1195 1200
 Arg Pro Pro Thr Thr Ala Thr Asn Met Asp Arg Pro Arg Thr Pro Gly
 1205 1210 1215
 His Gln Gln Pro Ser Lys Ser Cys Asp Ser Gln Pro Cys Leu His Gly
 1220 1225 1230
 Gly Thr Cys Gln Asp Gln Asp Ser Gly Lys Gly Phe Thr Cys Ser Cys
 1235 1240 1245
 Thr Ala Gly Arg Gly Ser Val Cys Glu Lys Val Gln Pro Pro Ser
 1250 1255 1260
 Met Pro Ala Phe Lys Gly His Ser Phe Leu Ala Phe Pro Thr Leu Arg
 1265 1270 1275 1280
 Ala Tyr His Thr Leu Arg Leu Ala Leu Glu Phe Arg Ala Leu Glu Thr
 1285 1290 1295
 Glu Gly Leu Leu Leu Tyr Asn Gly Asn Ala Arg Gly Lys Asp Phe Leu
 1300 1305 1310
 Ala Leu Ala Leu Leu Asp Gly Arg Val Gln Phe Arg Phe Asp Thr Gly
 1315 1320 1325
 Ser Gly Pro Ala Val Leu Thr Ser Leu Val Pro Val Glu Pro Gly Arg
 1330 1335 1340
 Trp His Arg Leu Glu Leu Ser Arg His Trp Arg Gln Gly Thr Leu Ser
 1345 1350 1355 1360
 Val Asp Gly Glu Thr Pro Val Val Gly Glu Ser Pro Ser Gly Thr Asp
 1365 1370 1375
 Gly Leu Asn Leu Asp Thr Asn Leu Tyr Val Gly Gly Ile Pro Glu Glu
 1380 1385 1390
 Gln Val Ala Met Val Leu Asp Arg Thr Ser Val Gly Val Gly Leu Lys
 1395 1400 1405
 Gly Cys Ile Arg Met Leu Asp Ile Asn Asn Gln Gln Leu Glu Leu Ser
 1410 1415 1420
 Asp Trp Gln Arg Ala Ala Val Gln Ser Ser Gly Val Gly Glu Cys Gly
 1425 1430 1435 1440
 Asp His Pro Cys Leu Pro Asn Pro Cys His Gly Gly Ala Leu Cys Gln
 1445 1450 1455
 Ala Leu Glu Ala Gly Met Phe Leu Cys Gln Cys Pro Pro Gly Arg Phe
 1460 1465 1470

Gly Pro Thr Cys Ala Asp Glu Lys Ser Pro Cys Gln Pro Asn Pro Cys
 1475 1480 1485
 His Gly Ala Ala Pro Cys Arg Val Leu Ser Ser Gly Gly Ala Lys Cys
 1490 1495 1500
 Glu Cys Pro Leu Gly Arg Ser Gly Thr Phe Cys Gln Thr Val Leu Glu
 1505 1510 1515 1520
 Thr Ala Gly Ser Arg Pro Phe Leu Ala Asp Phe Asn Gly Phe Ser Tyr
 1525 1530 1535
 Leu Glu Leu Lys Gly Leu His Thr Phe Glu Arg Asp Leu Gly Glu Lys
 1540 1545 1550
 Met Ala Leu Glu Met Val Phe Leu Ala Arg Gly Pro Ser Gly Leu Leu
 1555 1560 1565
 Leu Tyr Asn Gly Gln Lys Thr Asp Gly Lys Gly Asp Phe Val Ser Leu
 1570 1575 1580
 Ala Leu His Asn Arg His Leu Glu Phe Cys Tyr Asp Leu Gly Lys Gly
 1585 1590 1595 1600
 Ala Ala Val Ile Arg Ser Lys Glu Pro Ile Ala Leu Gly Thr Trp Val
 1605 1610 1615
 Arg Val Phe Leu Glu Arg Asn Gly Arg Lys Gly Ala Leu Gln Val Gly
 1620 1625 1630
 Asp Gly Pro Arg Val Leu Gly Glu Ser Pro Lys Ser Arg Lys Val Pro
 1635 1640 1645
 His Thr Met Leu Asn Leu Lys Glu Pro Leu Tyr Ile Gly Gly Ala Pro
 1650 1655 1660
 Asp Phe Ser Lys Leu Ala Arg Gly Ala Ala Val Ser Ser Gly Phe Ser
 1665 1670 1675 1680
 Gly Val Ile Gln Leu Val Ser Leu Arg Gly His Gln Leu Leu Thr Gln
 1685 1690 1695
 Glu His Val Leu Arg Ala Val Asp Val Ser Pro Phe Ala Asp His Pro
 1700 1705 1710
 Cys Thr Gln Ala Leu Gly Asn Pro Cys Leu Asn Gly Gly Ser Cys Val
 1715 1720 1725
 Pro Arg Glu Ala Thr Tyr Glu Cys Leu Cys Pro Gly Gly Phe Ser Gly
 1730 1735 1740
 Leu His Cys Glu Lys Gly Leu Val Glu Lys Ser Val Gly Asp Leu Glu
 1745 1750 1755 1760
 Thr Leu Ala Phe Asp Gly Arg Thr Tyr Ile Glu Tyr Leu Asn Ala Val
 1765 1770 1775
 Ile Glu Ser Glu Lys Ala Leu Gln Ser Asn His Phe Glu Leu Ser Leu
 1780 1785 1790

Arg Thr Glu Ala Thr Gln Gly Leu Val Leu Trp Ile Gly Lys Ala Ala
 1795 1800 1805

Glu Arg Ala Asp Tyr Met Ala Leu Ala Ile Val Asp Gly His Leu Gln
 1810 1815 1820

Leu Ser Tyr Asp Leu Gly Ser Gln Pro Val Val Leu Arg Ser Thr Val
 1825 1830 1835 1840

Lys Val Asn Thr Asn Arg Trp Leu Arg Ile Arg Ala His Arg Glu His
 1845 1850 1855

Arg Glu Gly Ser Leu Gln Val Gly Asn Glu Ala Pro Val Thr Gly Ser
 1860 1865 1870

Ser Pro Leu Gly Ala Thr Gln Leu Asp Thr Asp Gly Ala Leu Trp Leu
 1875 1880 1885

Gly Gly Leu Gln Lys Leu Pro Val Gly Gln Ala Leu Pro Lys Ala Tyr
 1890 1895 1900

Gly Thr Gly Phe Val Gly Cys Leu Arg Asp Val Val Val Gly His Arg
 1905 1910 1915 1920

Gln Leu His Leu Leu Glu Asp Ala Val Thr Lys Pro Glu Leu Arg Pro
 1925 1930 1935

Cys Pro Thr Pro
 1940

<210> 35
 <211> 1479
 <212> DNA
 <213> Homo sapiens

<400> 35
 atgtctgcac ttctgatcct agctcttgg ggagctgcag ttgctgacta caaagacgat 60
 gacgacaaga agagccctg ccagcccaac ccctgcccatt gggcgccgccc ctgcccgtgtg 120
 ctgcccggagg gtggtgctca gtgcgagtgc cccctggggc gtgagggcac cttctgcccag 180
 acagcctcgg ggcaggacgg ctctgggccc ttccctggctg acttcaacgg cttctcccac 240
 ctggagctga gaggcctgca caccttgcg cgggacctgg gggagaagat ggcgctggag 300
 gtctgttcc tggcacgagg ccccaagcggc ctcctgctct acaacggca gaagacggac 360
 ggcaagggggg acttcgtgtc gctggactg cgggaccggc gcctggagtt ccgctacgac 420
 ctgggcaagg gggcagcggg catcaggagc agggagccag tcaccctggg agcctggacc 480
 agggcttcac tggagcggaaa cggccgcgaag ggtccccctgc gtgtggcga cggcccccgt 540
 gtgttggggg agtccccgaa atcccgcaag gttccgcaca cctgtctcaa cctgaaggag 600
 cccgtctacg tagggggcgc tcccgacttc agcaagctgg cccgtctacg tgccgtgtcc 660
 tctggcttcg acggcgccat ccagctggc tccctcgagg gccgcacgt gctgaccccg 720
 gggcacgtgc tgccgcagggt ggacgtcactg tccttgcag gtcacccctg caccggggcc 780
 tcaggccacc cctgcctcaa tggggcctcc tgcgtcccga gggaggctgc ctatgtgtgc 840
 ctgtgtcccg ggggattctc aggaccgcac tgcgagaagg ggctgggtga gaagtcaacg 900
 ggggacgtgg ataccttggc ctttgacggg cggacctttg tcgagttacca caccgtgtg 960
 accggagagcg aactggccaa tgagatcccc gtcgagaagg cactgcacgg caaccacttt 1020
 gaactgagcc tgcgcactga ggccacgcac gggctgggtgc tctggagttgg caaggccacg 1080
 gagcggggcag actatgtggc actggccatt gtggacgggc acctgcaact gagctacaac 1140
 ctgggctccc agcccggttgc gctgcgttcc accgtgcggc tcaacaccaa cccgtgggtt 1200
 cgggtcggttgc cacataggga gcagagggaa ggtttccctgc aggtgggcaa tgaggccct 1260
 gtgacccggct cctcccccgt gggcgccacg cagctggaca ctgatggagc cctgtggctt 1320
 gggggcctgc cggagctgccc cgtggccca gcactgccc aaggcctacgg cacaggcttt 1380

gtgggctgct tgcgggacgt ggtggtgggc cggcaccgc tcgcacctgct ggaggacgcc 1440
 gtcaccaagc cagagctgct gcccgtcccc accccatga 1479

<210> 36
 <211> 492
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Asp
 1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Lys Ser Pro Cys Gln Pro Asn Pro Cys
 20 25 30

His Gly Ala Ala Pro Cys Arg Val Leu Pro Glu Gly Gly Ala Gln Cys
 35 40 45

Glu Cys Pro Leu Gly Arg Glu Gly Thr Phe Cys Gln Thr Ala Ser Gly
 50 55 60

Gln Asp Gly Ser Gly Pro Phe Leu Ala Asp Phe Asn Gly Phe Ser His
 65 70 75 80

Leu Glu Leu Arg Gly Leu His Thr Phe Ala Arg Asp Leu Gly Glu Lys
 85 90 95

Met Ala Leu Glu Val Val Phe Leu Ala Arg Gly Pro Ser Gly Leu Leu
 100 105 110

Leu Tyr Asn Gly Gln Lys Thr Asp Gly Lys Gly Asp Phe Val Ser Leu
 115 120 125

Ala Leu Arg Asp Arg Arg Leu Glu Phe Arg Tyr Asp Leu Gly Lys Gly
 130 135 140

Ala Ala Val Ile Arg Ser Arg Glu Pro Val Thr Leu Gly Ala Trp Thr
 145 150 155 160

Arg Val Ser Leu Glu Arg Asn Gly Arg Lys Gly Ala Leu Arg Val Gly
 165 170 175

Asp Gly Pro Arg Val Leu Gly Glu Ser Pro Lys Ser Arg Lys Val Pro
 180 185 190

His Thr Val Leu Asn Leu Lys Glu Pro Leu Tyr Val Gly Gly Ala Pro
 195 200 205

Asp Phe Ser Lys Leu Ala Arg Ala Ala Ala Val Ser Ser Gly Phe Asp
 210 215 220

Gly Ala Ile Gln Leu Val Ser Leu Gly Gly Arg Gln Leu Leu Thr Pro
 225 230 235 240

Glu His Val Leu Arg Gln Val Asp Val Thr Ser Phe Ala Gly His Pro
 245 250 255

Cys Thr Arg Ala Ser Gly His Pro Cys Leu Asn Gly Ala Ser Cys Val
 260 265 270

Pro Arg Glu Ala Ala Tyr Val Cys Leu Cys Pro Gly Gly Phe Ser Gly
 275 280 285
 Pro His Cys Glu Lys Gly Leu Val Glu Lys Ser Ala Gly Asp Val Asp
 290 295 300
 Thr Leu Ala Phe Asp Gly Arg Thr Phe Val Glu Tyr Leu Asn Ala Val
 305 310 315 320
 Thr Glu Ser Glu Leu Ala Asn Glu Ile Pro Val Glu Lys Ala Leu Gln
 325 330 335
 Ser Asn His Phe Glu Leu Ser Leu Arg Thr Glu Ala Thr Gln Gly Leu
 340 345 350
 Val Leu Trp Ser Gly Lys Ala Thr Glu Arg Ala Asp Tyr Val Ala Leu
 355 360 365
 Ala Ile Val Asp Gly His Leu Gln Leu Ser Tyr Asn Leu Gly Ser Gln
 370 375 380
 Pro Val Val Leu Arg Ser Thr Val Pro Val Asn Thr Asn Arg Trp Leu
 385 390 395 400
 Arg Val Val Ala His Arg Glu Gln Arg Glu Gly Ser Leu Gln Val Gly
 405 410 415
 Asn Glu Ala Pro Val Thr Gly Ser Ser Pro Leu Gly Ala Thr Gln Leu
 420 425 430
 Asp Thr Asp Gly Ala Leu Trp Leu Gly Gly Leu Pro Glu Leu Pro Val
 435 440 445
 Gly Pro Ala Leu Pro Lys Ala Tyr Gly Thr Gly Phe Val Gly Cys Leu
 450 455 460
 Arg Asp Val Val Val Gly Arg His Pro Leu His Leu Leu Glu Asp Ala
 465 470 475 480
 Val Thr Lys Pro Glu Leu Arg Pro Cys Pro Thr Pro
 485 490